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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/844,268

DATE: 01/28/2002

TIME: 11:28:19

Input Set : N:\Crf3\RULE60\09844268.raw

Output Set: N:\CRF3\01282002\I844268.raw

1 <110> APPLICANT: BOSWORTH, BRAD
2 VOGELI, PETER
3 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
4 RESISTANT TO F18 E. COLI ASSOCIATED DISEASES
5 <130> FILE REFERENCE: 21419/90368
6 <140> CURRENT APPLICATION NUMBER: 09/844,268
7 <141> CURRENT FILING DATE: 2001-04-27
8 <150> PRIOR APPLICATION NUMBER: 09/443,766
9 <151> PRIOR FILING DATE: 1999-11-19
12 <160> NUMBER OF SEQ ID NOS: 13
13 <170> SOFTWARE: PatentIn Ver. 2.0
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 20
17 <212> TYPE: DNA
18 <213> ORGANISM: Artificial Sequence
19 <220> FEATURE:
20 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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27 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
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35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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44 <212> TYPE: DNA
45 <213> ORGANISM: Artificial Sequence
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48 <400> SEQUENCE: 4
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53 <212> TYPE: DNA
54 <213> ORGANISM: Artificial Sequence
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56 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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61 <211> LENGTH: 23
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence
64 <220> FEATURE:
65 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
66 <400> SEQUENCE: 6
67     ctgcctgaac gtctatcaag atc 23
69 <210> SEQ ID NO: 7
70 <211> LENGTH: 22
71 <212> TYPE: DNA
72 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
75 <400> SEQUENCE: 7
76     agagtttcct catgcccaca gg 22
78 <210> SEQ ID NO: 8
79 <211> LENGTH: 22
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
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85     ctgctacagg accaccagca tc 22
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88 <211> LENGTH: 35
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
92 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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94     accagcagcg caaagtcctt gacgggcacg gcctc 35
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98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
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103     ctccctgtgc cttggaagtg at 22
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115 <211> LENGTH: 1269
116 <212> TYPE: DNA
117 <213> ORGANISM: Porcine
118 <220> FEATURE:
119 <221> NAME/KEY: CDS
120 <222> LOCATION: (9)..(1103)
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123      Met Trp Val Pro Ser Arg Arg His Leu Cys Leu Thr Phe Leu
124      1              5              10
125      cta gtc tgt gtt tta gca gca att ttc ttc ctg aac gtc tat caa gac  98
126      Leu Val Cys Val Leu Ala Ala Ile Phe Phe Leu Asn Val Tyr Gln Asp
127      15              20              25              30
128      ctc ttt tac agt ggc tta gac ctg ctg gcc ctg tgt cca gac cat aac  146
129      Leu Phe Tyr Ser Gly Leu Asp Leu Leu Ala Leu Cys Pro Asp His Asn
130      35              40              45
131      gtg gta tca tct ccc gtg gcc ata ttc tgc ctg gcg ggc acg ccg gta  194
132      Val Val Ser Ser Pro Val Ala Ile Phe Cys Leu Ala Gly Thr Pro Val
133      50              55              60
134      cac ccc aac gcc tcc gat tcc tgt ccc aag cat cct gcc tcc ttt tcc  242
135      His Pro Asn Ala Ser Asp Ser Cys Pro Lys His Pro Ala Ser Phe Ser
136      65              70              75
137      ggg acc tgg act att tac ccg gat ggc cgg ttt ggg aac cag atg gga  290
138      Gly Thr Trp Thr Ile Tyr Pro Asp Gly Arg Phe Gly Asn Gln Met Gly
139      80              85              90
140      cag tat gcc acg ctg ctg gcc ctg gcg cag ctc aac ggc cgc cag gcc  338
141      Gln Tyr Ala Thr Leu Leu Ala Leu Ala Gln Leu Asn Gly Arg Gln Ala
142      95              100              105              110
143      ttc atc cag cct gcc atg cac gcc gtc ctg gcc ccc gtg ttc cgc atc  386
144      Phe Ile Gln Pro Ala Met His Ala Val Leu Ala Pro Val Phe Arg Ile
145      115              120              125
146      acg ctg cct gtc ctg gcg ccc gag gta gac agg cac gct cct tgg cgg  434
147      Thr Leu Pro Val Leu Ala Pro Glu Val Asp Arg His Ala Pro Trp Arg
148      130              135              140
149      gag ctg gag ett cac gac tgg atg tcc gag gat tat gcc cac tta aag  482
150      Glu Leu Glu Leu His Asp Trp Met Ser Glu Asp Tyr Ala His Leu Lys
151      145              150              155
152      gag ccc tgg ctg aag ctc acc ggc ttc ccc tgc tcc tgg acc ttc ttc  530
153      Glu Pro Trp Leu Lys Leu Thr Gly Phe Pro Cys Ser Trp Thr Phe Phe
154      160              165              170
155      cac cac ctc cgg gag cag atc cgc agc gag ttc acc ctg cac gac cac  578

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156   His His Leu Arg Glu Gln Ile Arg Ser Glu Phe Thr Leu His Asp His
157   175                               180                               185                               190
158   ctt cgg caa gag gcc cag ggg gta ctg agt cag ttc cgt cta ccc cgc      626
159   Leu Arg Gln Glu Ala Gln Gly Val Leu Ser Gln Phe Arg Leu Pro Arg
160                               195                               200                               205
161   aca ggg gac cgc ccc agc acc ttc gtg ggg gtc cac gtg cgc cgc ggg      674
162   Thr Gly Asp Arg Pro Ser Thr Phe Val Gly Val His Val Arg Arg Gly
163                               210                               215                               220
164   gac tat ctg cgt gtg atg ccc aag cgc tgg aag ggg gtg gtg ggt gac      722
165   Asp Tyr Leu Arg Val Met Pro Lys Arg Trp Lys Gly Val Val Gly Asp
166                               225                               230                               235
167   ggc cgt tac ctc cag cag gct atg gac tgg ttc cgg gcc cga tac gaa      770
168   Gly Arg Tyr Leu Gln Gln Ala Met Asp Trp Phe Arg Ala Arg Tyr Glu
169                               240                               245                               250
170   gcc ccc gtc ttt gtg gtc acc agc aac ggc atg gag tgg tgc cgg aag      818
171   Ala Pro Val Phe Val Val Thr Ser Asn Gly Met Glu Trp Cys Arg Lys
172   255                               260                               265                               270
173   aac atc gac acc tcc cgg ggg gac gtg atc ttt gct ggc gat ggg cgg      866
174   Asn Ile Asp Thr Ser Arg Gly Asp Val Ile Phe Ala Gly Asp Gly Arg
175                               275                               280                               285
176   gag gcc gcg ccc gcc agg gac ttt gcg ctg ctg gtg cag tgc aac cac      914
177   Glu Ala Ala Pro Ala Arg Asp Phe Ala Leu Leu Val Gln Cys Asn His
178                               290                               295                               300
179   acc atc atg acc att ggc acc ttc ggc ttc tgg gcc gcc tac ctg gct      962
180   Thr Ile Met Thr Ile Gly Thr Phe Gly Phe Trp Ala Ala Tyr Leu Ala
181                               305                               310                               315
182   ggt gga gat acc atc tac ttg gct aac ttc acc ctg ccc act tcc agc      1010
183   Gly Gly Asp Thr Ile Tyr Leu Ala Asn Phe Thr Leu Pro Thr Ser Ser
184   320                               325                               330
185   ttc ctg aag atc ttt aaa ccc gag gct gcc ttc ctg ccc gag tgg gtg      1058
186   Phe Leu Lys Ile Phe Lys Pro Glu Ala Ala Phe Leu Pro Glu Trp Val
187   335                               340                               345                               350
188   ggc att aat gca gac ttg tct cca ctc cag atg ttg gct ggg cct      1103
189   Gly Ile Asn Ala Asp Leu Ser Pro Leu Gln Met Leu Ala Gly Pro
190                               355                               360                               365
191   tgaaccagcc aggagccttt ctggaatagc ctgggtcaac ccagggccag cgttatgggt 1163
192   ctccggaagc ccgagtaact tccggagatg ctgggtggtcc tgtagcaggc tggacactta 1223
193   tttcaagagt gattctaatt ggctggactc agaggaaacc ctgcag      1269
195 <210> SEQ ID NO: 13
196 <211> LENGTH: 365
197 <212> TYPE: PRT
198 <213> ORGANISM: Porcine
199 <400> SEQUENCE: 13
200   Met Trp Val Pro Ser Arg Arg His Leu Cys Leu Thr Phe Leu Leu Val
201       1                               5                               10                               15
202   Cys Val Leu Ala Ala Ile Phe Phe Leu Asn Val Tyr Gln Asp Leu Phe
203                               20                               25                               30
204   Tyr Ser Gly Leu Asp Leu Leu Ala Leu Cys Pro Asp His Asn Val Val
205       35                               40                               45

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206   Ser Ser Pro Val Ala Ile Phe Cys Leu Ala Gly Thr Pro Val His Pro
207       50              55              60
208   Asn Ala Ser Asp Ser Cys Pro Lys His Pro Ala Ser Phe Ser Gly Thr
209       65              70              75              80
210   Trp Thr Ile Tyr Pro Asp Gly Arg Phe Gly Asn Gln Met Gly Gln Tyr
211              85              90              95
212   Ala Thr Leu Leu Ala Leu Ala Gln Leu Asn Gly Arg Gln Ala Phe Ile
213              100             105             110
214   Gln Pro Ala Met His Ala Val Leu Ala Pro Val Phe Arg Ile Thr Leu
215              115             120             125
216   Pro Val Leu Ala Pro Glu Val Asp Arg His Ala Pro Trp Arg Glu Leu
217              130             135             140
218   Glu Leu His Asp Trp Met Ser Glu Asp Tyr Ala His Leu Lys Glu Pro
219              145             150             155             160
220   Trp Leu Lys Leu Thr Gly Phe Pro Cys Ser Trp Thr Phe Phe His His
221              165             170             175
222   Leu Arg Glu Gln Ile Arg Ser Glu Phe Thr Leu His Asp His Leu Arg
223              180             185             190
224   Gln Glu Ala Gln Gly Val Leu Ser Gln Phe Arg Leu Pro Arg Thr Gly
225              195             200             205
226   Asp Arg Pro Ser Thr Phe Val Gly Val His Val Arg Arg Gly Asp Tyr
227              210             215             220
228   Leu Arg Val Met Pro Lys Arg Trp Lys Gly Val Val Gly Asp Gly Arg
229              225             230             235             240
230   Tyr Leu Gln Gln Ala Met Asp Trp Phe Arg Ala Arg Tyr Glu Ala Pro
231              245             250             255
232   Val Phe Val Val Thr Ser Asn Gly Met Glu Trp Cys Arg Lys Asn Ile
233              260             265             270
234   Asp Thr Ser Arg Gly Asp Val Ile Phe Ala Gly Asp Gly Arg Glu Ala
235              275             280             285
236   Ala Pro Ala Arg Asp Phe Ala Leu Leu Val Gln Cys Asn His Thr Ile
237              290             295             300
238   Met Thr Ile Gly Thr Phe Gly Phe Trp Ala Ala Tyr Leu Ala Gly Gly
239              305             310             315             320
240   Asp Thr Ile Tyr Leu Ala Asn Phe Thr Leu Pro Thr Ser Ser Phe Leu
241              325             330             335
242   Lys Ile Phe Lys Pro Glu Ala Ala Phe Leu Pro Glu Trp Val Gly Ile
243              340             345             350
244   Asn Ala Asp Leu Ser Pro Leu Gln Met Leu Ala Gly Pro
245              355             360             365

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